

SEQUENCE LISTING

<110> BANYU PHARMACEUTICAL CO., LTD.

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)

BINDING PROTEIN-COUPLED RECEPTOR PROTEIN, BG3

<130> B1-101PCT

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<150> JP 1999-82641

<151> 1999-03-25

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

T09250"992E9660

synthesized primer sequence

<400> 1

batngccaac ctbkccttct c

21

<210> 2

<211> 3117

<212> DNA

<213> Homo sapiens

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gccgtgctgt cctccgtgag caccatccgg aaccagcgct accacatcca cgccaacctg 120

tccttcgccg tgctggtggc ccaggctctg ctgctcatta gtttcgcct cgagccgggc 180

acgacccccct gccaaagtgat ggccgtgctc ctacactact tcttcctgag tgccttcgca 240

tggatgctgg tggaggggct gcacctctac agcatggtga tcaaggctct tgggtcggag 300

gacagcaagc accgttacta ctatgggatg ggatgggggtt ttctcttct gatctgcac 360

atttcaactgt catttgccat ggacagttac ggaacaagca acaattgctg gctgtcgttg 420

FOI b6 b7C 9903660

gcgagtggcg ccactcgggc ctttctagcc cctgccctgt ttgtcatcgt ggtcaacatt 480

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catggagacc ccagtgcctt caagttgacg gccaaaggcag tggccgtgct gctgcccac 600

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tacatgtttg ccacgtcaa ctccctgcag ggactgttca tattcctctt tcattgtctc 720

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tttggccaaa aataagaaat tggaaagaat gaaatgttta gtttatagta gaagaaagat 3060

gatgacacta agttgtgaaa atatgttgtg atttttatga aataaactca tgtcctg 3117

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 3

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<210> 4

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

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ctgctcgtga gcgaccagac c

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<210> 5

<211> 5340

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (517).. (3138)

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cgctccaggg gaaaaccacg cacaaaacct tcttcagaga aaagggaagc tccaaacctg 120

105260" 994E9560

actgagacaa acggaggctc ttgaaataaa aagaaaatac cgcaggacaa acagcctccc 180

gtccccgggc gcaggtcgcg gtcacagtgg tgacctggga ttgctttccc aggactgcga 240

gtcgggtttg ggtttctcct ccctgcattc cacagctgct ctggtcacg caacgtgttt 300

attgatcact gaagaatctc aagttttgag acgaggaaga aacacccatt aggtctccaa 360

gacagctgtg tttcaciaaac tttagggaga cagaaatttt ctcccctgga acctgtgaaa 420

atgtcccttt tccaaggaag tgaaggttaa gaggtcccg tctcacagac cctcagtaat 480

ttcaattggc tccgagcttt gacctccgag agagcc atg gaa aag ctg ctg cgg 534

Met Glu Lys Leu Leu Arg

1

5

ctg tgc tgc tgg tac tcc tgg ctg ctg cta ttt tat tac aac ttt cag 582

Leu Cys Cys Trp Tyr Ser Trp Leu Leu Leu Phe Tyr Tyr Asn Phe Gln

10

15

20

gtg cgt ggc gtc tac tcc aga tcg cag gac cat cca gga ttt cag gtg 630

Val Arg Gly Val Tyr Ser Arg Ser Gln Asp His Pro Gly Phe Gln Val

25

30

35

ttg gcg tct gct tcc cat tac tgg cca ctg gag aat gtg gat ggg atc 678

099269660

Leu Ala Ser Ala Ser His Tyr Trp Pro Leu Glu Asn Val Asp Gly Ile

40

45

50

cat gaa ctt cag gat aca act gga gat att gtg gaa ggg aag gtc aac 726

His Glu Leu Gln Asp Thr Thr Gly Asp Ile Val Glu Gly Lys Val Asn

55

60

65

70

aaa ggc att tac ctg aaa gag gaa aag gga gtc acg ctt ctc tat tac 774

Lys Gly Ile Tyr Leu Lys Glu Glu Lys Gly Val Thr Leu Leu Tyr Tyr

75

80

85

ggc agg tac aac agc tcc tgc atc agc aag cca gag cag tgt ggc cct 822

Gly Arg Tyr Asn Ser Ser Cys Ile Ser Lys Pro Glu Gln Cys Gly Pro

90

95

100

gaa ggg gtc acg ttt tct ttt ttc tgg aag aca caa gga gaa cag tct 870

Glu Gly Val Thr Phe Ser Phe Phe Trp Lys Thr Gln Gly Glu Gln Ser

105

110

115

aga cca atc cct tct gcg tat ggg gga cag gtc atc tcc aat ggg ttc 918

Arg Pro Ile Pro Ser Ala Tyr Gly Gly Gln Val Ile Ser Asn Gly Phe

120

125

130

aaa gtc tgc tcc agc ggt ggc aga ggc tct gtg gag ctg tac acg cgg 966

Lys Val Cys Ser Ser Gly Gly Arg Gly Ser Val Glu Leu Tyr Thr Arg

135

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145

150

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gac aat tcc atg aca tgg gag gcc tcc ttc agc ccc cca ggc ccc tat 1014

Asp Asn Ser Met Thr Trp Glu Ala Ser Phe Ser Pro Pro Gly Pro Tyr

155

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165

tgg act cat gtc cta ttt aca tgg aaa tcc aag gag ggc ctg aaa gtc 1062

Trp Thr His Val Leu Phe Thr Trp Lys Ser Lys Glu Gly Leu Lys Val

170

175

180

tac gtc aac ggg acc ctg agc acc tct gat ccg agt gga aaa gtg tct 1110

Tyr Val Asn Gly Thr Leu Ser Thr Ser Asp Pro Ser Gly Lys Val Ser

185

190

195

cgt gac tat gga gag tcc aac gtc aac ctc gtg ata ggg tct gag cag 1158

Arg Asp Tyr Gly Glu Ser Asn Val Asn Leu Val Ile Gly Ser Glu Gln

200

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210

gac cag gcc aag tgt tat gag aac ggt gct ttc gat gag ttc atc atc 1206

Asp Gln Ala Lys Cys Tyr Glu Asn Gly Ala Phe Asp Glu Phe Ile Ile

215

220

225

230

tgg gag cgg gct ctg act ccg gat gag atc gcc atg tac ttc act gct 1254

Trp Glu Arg Ala Leu Thr Pro Asp Glu Ile Ala Met Tyr Phe Thr Ala

235

240

245

gcc att gga aag cat gct tta ttg tct tca acg ctg cca agc ctc ttc 1302

00963766-002501

Ala Ile Gly Lys His Ala Leu Leu Ser Ser Thr Leu Pro Ser Leu Phe

250

255

260

atg aca tcc aca gca agc ccc gtg atg ccc aca gat gcc tac cat ccc 1350

Met Thr Ser Thr Ala Ser Pro Val Met Pro Thr Asp Ala Tyr His Pro

265

270

275

atc ata acc aac ctg aca gaa gag aga aaa acc ttc caa agt ccc gga 1398

Ile Ile Thr Asn Leu Thr Glu Glu Arg Lys Thr Phe Gln Ser Pro Gly

280

285

290

gtg ata ctg agt tac ctc caa aat gta tcc ctc agc tta ccc agt aag 1446

Val Ile Leu Ser Tyr Leu Gln Asn Val Ser Leu Ser Leu Pro Ser Lys

295

300

305

310

tcc ctc tcg gag cag aca gcc ttg aat ctc acc aag acc ttc tta aaa 1494

Ser Leu Ser Glu Gln Thr Ala Leu Asn Leu Thr Lys Thr Phe Leu Lys

315

320

325

gcc gtg gga gag atc ctt cta ctg cct ggt tgg att gct ctg tca gag 1542

Ala Val Gly Glu Ile Leu Leu Leu Pro Gly Trp Ile Ala Leu Ser Glu

330

335

340

gac agc gcc gtg gta ctg agt ctc atc gac act att gac acc gtc atg 1590

Asp Ser Ala Val Val Leu Ser Leu Ile Asp Thr Ile Asp Thr Val Met

345

350

355

09963766-092501

ggc cat gta tcc tcc aac ctg cac ggc agc acg ccc cag gtc acc gtg 1638

Gly His Val Ser Ser Asn Leu His Gly Ser Thr Pro Gln Val Thr Val

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365

370

gag ggc tcc tct gcc atg gca gag ttt tcc gtg gcc aaa atc ctg ccc 1686

Glu Gly Ser Ser Ala Met Ala Glu Phe Ser Val Ala Lys Ile Leu Pro

375

380

385

390

aag acc gtg aat tcc tcc cat tac cgc ttc ccg gcc cac ggg cag agc 1734

Lys Thr Val Asn Ser Ser His Tyr Arg Phe Pro Ala His Gly Gln Ser

395

400

405

ttc atc cag atc ccc cac gag gcc ttc cac agg cac gcc tgg agc acc 1782

Phe Ile Gln Ile Pro His Glu Ala Phe His Arg His Ala Trp Ser Thr

410

415

420

gtc gtg ggt ctg ctg tac cac agc atg cac tac tac ctg aac aac atc 1830

Val Val Gly Leu Leu Tyr His Ser Met His Tyr Tyr Leu Asn Asn Ile

425

430

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tgg ccc gcc cac acc aag atc gcg gag gcc atg cat cac cag gac tgc 1878

Trp Pro Ala His Thr Lys Ile Ala Glu Ala Met His His Gln Asp Cys

440

445

450

ctg ctg ttc gcc acc agc cac ctg att tcc ctg gag gtg tcc cca cca 1926

009637E 0950
T05260 994E9660

Leu Leu Phe Ala Thr Ser His Leu Ile Ser Leu Glu Val Ser Pro Pro

455

460

465

470

ccc acc ctg tct cag aac ctg tgc ggc tct cca ctc att acg gtc cac 1974

Pro Thr Leu Ser Gln Asn Leu Ser Gly Ser Pro Leu Ile Thr Val His

475

480

485

ctc aag cac aga ttg aca cgt aag cag cac agt gag gcc acc aac agc 2022

Leu Lys His Arg Leu Thr Arg Lys Gln His Ser Glu Ala Thr Asn Ser

490

495

500

agc aac cga gtc ttc gtg tac tgc gcc ttc ctg gac ttc agc tcc gga 2070

Ser Asn Arg Val Phe Val Tyr Cys Ala Phe Leu Asp Phe Ser Ser Gly

505

510

515

gaa ggg gtc tgg tgc aac cac ggc tgt gcg ctc acg aga gga aac ctc 2118

Glu Gly Val Trp Ser Asn His Gly Cys Ala Leu Thr Arg Gly Asn Leu

520

525

530

acc tac tcc gtc tgc cgc tgc act cac ctc acc aac ttt gcc atc ctc 2166

Thr Tyr Ser Val Cys Arg Cys Thr His Leu Thr Asn Phe Ala Ile Leu

535

540

545

550

atg cag gtg gtc ccg ctg gag ctt gca cgc gga cac cag gtg gcg ctg 2214

Met Gln Val Val Pro Leu Glu Leu Ala Arg Gly His Gln Val Ala Leu

555

560

565

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 Ser Ser Ile Ser Tyr Val Gly Cys Ser Leu Ser Val Leu Cys Leu Val
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gcc acg ctg gtc acc ttc gcc gtg ctg tcc tcc gtg agc acc atc cgg 2310
 Ala Thr Leu Val Thr Phe Ala Val Leu Ser Ser Val Ser Thr Ile Arg
 585 590 595

aac cag cgc tac cac atc cac gcc aac ctg tcc ttc gcc gtg ctg gtg 2358
 Asn Gln Arg Tyr His Ile His Ala Asn Leu Ser Phe Ala Val Leu Val
 600 605 610

gcc cag gtc ctg ctg ctc att agt ttc cgc ctc gag ccg gcc acg acc 2406
 Ala Gln Val Leu Leu Leu Ile Ser Phe Arg Leu Glu Pro Gly Thr Thr
 615 620 625 630

ccc tgc caa gtg atg gcc gtg ctc cta cac tac ttc ttc ctg agt gcc 2454
 Pro Cys Gln Val Met Ala Val Leu Leu His Tyr Phe Phe Leu Ser Ala
 635 640 645

ttc gca tgg atg ctg gtg gag ggg ctg cac ctc tac agc atg gtg atc 2502
 Phe Ala Trp Met Leu Val Glu Gly Leu His Leu Tyr Ser Met Val Ile
 650 655 660

aag gtc ttt ggg tcg gag gac agc aag cac cgt tac tac tat ggg atg 2550

09963766-092501

Lys Val Phe Gly Ser Glu Asp Ser Lys His Arg Tyr Tyr Tyr Gly Met

665

670

675

gga tgg ggt ttt cct ctt ctg atc tgc atc att tca ctg tca ttt gcc 2598

Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile Ile Ser Leu Ser Phe Ala

680

685

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atg gac agt tac gga aca agc aac aat tgc tgg ctg tcg ttg gcg agt 2646

Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys Trp Leu Ser Leu Ala Ser

695

700

705

710

ggc gcc atc tgg gcc ttt gta gcc cct gcc ctg ttt gtc atc gtg gtc 2694

Gly Ala Ile Trp Ala Phe Val Ala Pro Ala Leu Phe Val Ile Val Val

715

720

725

aac att ggc atc ctc atc gct gtg acc aga gtc atc tca cag atc agc 2742

Asn Ile Gly Ile Leu Ile Ala Val Thr Arg Val Ile Ser Gln Ile Ser

730

735

740

gcc gac aac tac aag atc cat gga gac ccc agt gcc ttc aag ttg acg 2790

Ala Asp Asn Tyr Lys Ile His Gly Asp Pro Ser Ala Phe Lys Leu Thr

745

750

755

gcc aag gca gtg gcc gtg ctg ctg ccc atc ctg ggt acc tcg tgg gtc 2838

Ala Lys Ala Val Ala Val Leu Leu Pro Ile Leu Gly Thr Ser Trp Val

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765

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ttt gcc acg ctc aac tcc ctg cag gga ctg ttc ata ttc ctc ttt cat 2934
 Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu Phe Ile Phe Leu Phe His
 795 800 805

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 Cys Leu Leu Asn Ser Glu Val Arg Ala Ala Phe Lys His Lys Thr Lys
 810 815 820

gtc tgg tcg ctc acg agc agc tcc gcc cgc acc tcc aac gcg aag ccc 3030
 Val Trp Ser Leu Thr Ser Ser Ser Ala Arg Thr Ser Asn Ala Lys Pro
 825 830 835

ttc cac tcg gac ctc atg aat ggg acc cgg cca ggc atg gcc tcc acc 3078
 Phe His Ser Asp Leu Met Asn Gly Thr Arg Pro Gly Met Ala Ser Thr
 840 845 850

aag ctc agc cct tgg gac aag agc agc cac tct gcc cac cgc gtc gac 3126
 Lys Leu Ser Pro Trp Asp Lys Ser Ser His Ser Ala His Arg Val Asp
 855 860 865 870

ctg tca gcc gtg tgagccggga ggctgccaac caggccaggc tgcgctcaga 3178

T05260"99Z"99660

Leu Ser Ala Val

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5340

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<212> PRT

<213> Homo sapiens

<400> 6

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20

25

30

His Pro Gly Phe Gln Val Leu Ala Ser Ala Ser His Tyr Trp Pro Leu

35

40

45

Glu Asn Val Asp Gly Ile His Glu Leu Gln Asp Thr Thr Gly Asp Ile

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60

Val Glu Gly Lys Val Asn Lys Gly Ile Tyr Leu Lys Glu Glu Lys Gly

65

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75

80

Val Thr Leu Leu Tyr Tyr Gly Arg Tyr Asn Ser Ser Cys Ile Ser Lys

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Pro Glu Gln Cys Gly Pro Glu Gly Val Thr Phe Ser Phe Phe Trp Lys

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Thr Gln Gly Glu Gln Ser Arg Pro Ile Pro Ser Ala Tyr Gly Gly Gln

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Val Glu Leu Tyr Thr Arg Asp Asn Ser Met Thr Trp Glu Ala Ser Phe

145

150

155

160

Ser Pro Pro Gly Pro Tyr Trp Thr His Val Leu Phe Thr Trp Lys Ser

165

170

175

Lys Glu Gly Leu Lys Val Tyr Val Asn Gly Thr Leu Ser Thr Ser Asp

180

185

190

Pro Ser Gly Lys Val Ser Arg Asp Tyr Gly Glu Ser Asn Val Asn Leu

195

200

205

Val Ile Gly Ser Glu Gln Asp Gln Ala Lys Cys Tyr Glu Asn Gly Ala

210

215

220

Phe Asp Glu Phe Ile Ile Trp Glu Arg Ala Leu Thr Pro Asp Glu Ile

225

230

235

240

Ala Met Tyr Phe Thr Ala Ala Ile Gly Lys His Ala Leu Leu Ser Ser

245

250

255

00963766-092501
T05260"99269660

Thr Leu Pro Ser Leu Phe Met Thr Ser Thr Ala Ser Pro Val Met Pro
 260 265 270

Thr Asp Ala Tyr His Pro Ile Ile Thr Asn Leu Thr Glu Glu Arg Lys
 275 280 285

Thr Phe Gln Ser Pro Gly Val Ile Leu Ser Tyr Leu Gln Asn Val Ser
 290 295 300

Leu Ser Leu Pro Ser Lys Ser Leu Ser Glu Gln Thr Ala Leu Asn Leu
 305 310 315 320

Thr Lys Thr Phe Leu Lys Ala Val Gly Glu Ile Leu Leu Leu Pro Gly
 325 330 335

Trp Ile Ala Leu Ser Glu Asp Ser Ala Val Val Leu Ser Leu Ile Asp
 340 345 350

Thr Ile Asp Thr Val Met Gly His Val Ser Ser Asn Leu His Gly Ser
 355 360 365

Thr Pro Gln Val Thr Val Glu Gly Ser Ser Ala Met Ala Glu Phe Ser
 370 375 380

Val Ala Lys Ile Leu Pro Lys Thr Val Asn Ser Ser His Tyr Arg Phe

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 994E9660

385 390 395 400

Pro Ala His Gly Gln Ser Phe Ile Gln Ile Pro His Glu Ala Phe His

405 410 415

Arg His Ala Trp Ser Thr Val Val Gly Leu Leu Tyr His Ser Met His

420 425 430

Tyr Tyr Leu Asn Asn Ile Trp Pro Ala His Thr Lys Ile Ala Glu Ala

435 440 445

Met His His Gln Asp Cys Leu Leu Phe Ala Thr Ser His Leu Ile Ser

450 455 460

Leu Glu Val Ser Pro Pro Pro Thr Leu Ser Gln Asn Leu Ser Gly Ser

465 470 475 480

Pro Leu Ile Thr Val His Leu Lys His Arg Leu Thr Arg Lys Gln His

485 490 495

Ser Glu Ala Thr Asn Ser Ser Asn Arg Val Phe Val Tyr Cys Ala Phe

500 505 510

Leu Asp Phe Ser Ser Gly Glu Gly Val Trp Ser Asn His Gly Cys Ala

515 520 525

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575

590

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620

640

655

670

Arg Tyr Tyr Tyr Gly Met Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile
 675 680 685

Ile Ser Leu Ser Phe Ala Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys
 690 695 700

Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp Ala Phe Val Ala Pro Ala
 705 710 715 720

Leu Phe Val Ile Val Val Asn Ile Gly Ile Leu Ile Ala Val Thr Arg
 725 730 735

Val Ile Ser Gln Ile Ser Ala Asp Asn Tyr Lys Ile His Gly Asp Pro
 740 745 750

Ser Ala Phe Lys Leu Thr Ala Lys Ala Val Ala Val Leu Leu Pro Ile
 755 760 765

Leu Gly Thr Ser Trp Val Phe Gly Val Leu Ala Val Asn Gly Cys Ala
 770 775 780

Val Val Phe Gln Tyr Met Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu
 785 790 795 800

Phe Ile Phe Leu Phe His Cys Leu Leu Asn Ser Glu Val Arg Ala Ala

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805

810

815

Phe Lys His Lys Thr Lys Val Trp Ser Leu Thr Ser Ser Ser Ala Arg

820

825

830

Thr Ser Asn Ala Lys Pro Phe His Ser Asp Leu Met Asn Gly Thr Arg

835

840

845

Pro Gly Met Ala Ser Thr Lys Leu Ser Pro Trp Asp Lys Ser Ser His

850

855

860

Ser Ala His Arg Val Asp Leu Ser Ala Val

865

870

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